<210> 1
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 CDRH1

<400> 1
Asp Tyr Gly Met Asn
 1   5

<210> 2
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40/human hybrid CDRH2

<400> 2
Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val Lys
 1   5   10   15
Gly

<210> 3
<211> 9
<212> PRT
<213> Artificial Sequence

```
<220>
<223> hTNF40 CDRH3

<400> 3
Gly Tyr Arg Ser Tyr Ala Met Asp Tyr
 1               5


<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 CDRL1

<400> 4
Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
 1               5                   10


<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 CDRL2

<400> 5
Ser Ala Ser Phe Leu Tyr Ser
 1               5


<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 CDRL3

<400> 6
Gln Gln Tyr Asn Ile Tyr Pro Leu Thr
 1               5


<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 CDRH2

<400> 7
```

```
Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe Lys
 1               5                   10                  15
Gly



<210> 8
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS

<222> (1)...(321)
<223> hTNF40-gL1

<223> hTNF40-gL1

<400> 8
gac att caa atg acc cag agc cca tcc agc ctg agc gca tct gta gga    48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                   10                  15

gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac    96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
              20                  25                  30

gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc   144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
          35                  40                  45

tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga   192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
      50                  55                  60

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc   288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
                  85                  90                  95

aca ttc ggt cag ggt act aaa gta gaa atc aaa                       321
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                 100                 105



<210> 11
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(354)
```

<223> gh3hTNF40.4

<223> Grafted Heavy Chain for Modified Fab

<400> 11
gag gtt cag ctg gtc gag tca gga ggc ggt ctc gtg cag cct ggc gga   48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

tca ctg aga ttg tcc tgt gct gca tct ggt tac gtc ttc aca gac tat   96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr
            20   25   30

gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg   144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45

ggt tgg att aat act tac att gga gag cct att tat gct gac agc gtc   192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
    50   55   60

aag ggc aga ttc acg ttc tct cta gac aca tcc aag tca aca gca tac   240
Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65   70   75   80

ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt   288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc   336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            100   105   110

cta gtc aca gtc tcc tca   354
Leu Val Thr Val Ser Ser
        115

<210> 83
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework L1

<400> 83
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15
Asp Arg Val Thr Ile Thr Cys
            20

<210> 84
<211> 23
<212> PRT

<213> Artificial Sequence

<220>
<223> hTNF40 framework L1

<400> 84
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1   5   10   15
Asp Arg Val Ser Val Thr Cys
            20

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework L2

<400> 85
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1   5   10   15

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework L2

<400> 86
Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile Tyr
1   5   10   15

<210> 87
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework L3

<400> 87
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
            20   25   30

<210> 88
<211> 32
<212> PRT
<213> Artificial Sequence

```
<220>
<223> hTNF40 framework L3

<400> 88
Gly Val Pro Tyr Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1               5                  10                  15
Leu Thr Ile Ser Thr Val Gln Ser Glu Asp Leu Ala Glu Tyr Phe Cys
            20                  25                  30


<210> 89
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework L4

<400> 89
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 1               5                  10


<210> 90
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework L4

<400> 90
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 1               5                  10


<210> 91

<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework H1

<400> 91
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
            20                  25                  30


<210> 92
<211> 30
<212> PRT
<213> Artificial Sequence
```

<220>
<223> hTNF40 framework H1

<400> 92
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1   5   10   15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr
             20   25   30

<210> 93
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework H2

<400> 93
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1   5   10

<210> 94
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H2

<400> 94
Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met Gly
 1   5   10

<210> 95
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework H3

<400> 95
Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
             20   25   30

<210> 96
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> hTNF40 framework H3

<400> 96
Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe Leu Gln
1   5   10   15
Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg
            20   25   30

<210> 97
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework H4

<400> 97
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 98
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 1 consensus framework H4

<400> 98
Trp Gly Gln Gly Thr Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 99
<211> 324
<212> DNA
<213> murine

<220>
<221> CDS
<222> (1)...(324)
<223> mouse hTNF40 light chain variable domain

<400> 99
gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca gta gga   48
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1   5   10   15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat   96
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
            20   25   30

gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg aat   144

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Asn
        35                  40                  45

tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc   192
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly
        50                  55                  60

agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser
65                  70                  75                  80

gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc   288
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
                    85                  90                  95

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt                   324
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
            100                 105


<210> 100
<211> 354
<212> DNA
<213> murine

<220>
<221> CDS
<222> (1)...(354)
<223> mouse hTNF40 heavy chain variable domain

<400> 100
cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag    48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1                   5                  10                  15

aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat    96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr
                20                  25                  30

gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg   144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met
        35                  40                  45

ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc   192
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe
        50                  55                  60

aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt   240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
65                  70                  75                  80

ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt   288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
                    85                  90                  95

gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc   336
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
```

```
tca gtc acc gtc tct tca                                          354
Ser Val Thr Val Ser Ser
        115
```

<210> 101
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Ompa oligonucleotide adaptor

<221> CDS
<222> (29)...(0)
<223> 67

<400> 101
```
tcgagttcta gataacgagg cgtaaaaaat gaaaaagaca gctatcgcaa ttgcagtggc 60
cttggctctg acgtacgagt cagg                                       84
```

<210> 102
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (2)...(40)

<221> CDS
<222> (43)...(66)

<223> IGS cassette-1

<400> 102
```
g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt ta atg aag   48
  Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys   Met Lys
   1           5                 10                      15

aag act gct ata gca att g                                         67
Lys Thr Ala Ile Ala Ile
              20
```

<210> 103
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (2)...(43)

<221> CDS
<222> (45)...(68)

<223> IGS cassette-2

<400> 103
g agc tca cca gta aca aaa agt ttt aat aga ggg gag tgt taa   43
  Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
   1   5   10

a atg aag aag act gct ata gca att g   69
  Met Lys Lys Thr Ala Ile Ala Ile
       15   20

<210> 104
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (2)...(43)

<221> CDS
<222> (57)...(80)

<223> IGS cassette-3

<400> 104
g agc tca cca gta aca aaa agc ttt aat aga gga gag tgt tga   43
  Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
   1   5   10

ggaggaaaaa aaa atg aag aaa act gct ata gca att g   81
           Met Lys Lys Thr Ala Ile Ala Ile
                15   20

<210> 105
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (2)...(43)

<221> CDS
<222> (57)...(80)

<223> IGS cassette-4

<400> 105
g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt tga   43
  Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
   1   5   10

```
cgaggattat ata atg aag aaa act gct ata gca att g
           Met Lys Lys Thr Ala Ile Ala Ile
               15                  20
```

<210> 106
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 3 consensus framework H1

<400> 106

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5               10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
            20                  25                  30
```

<210> 107
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 3 consensus framework H2

<400> 107

```
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1               5               10
```

<210> 108
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 3 consensus framework H3

<400> 108

```
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 1               5               10                  15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20                  25                  30
```

<210> 109
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> human group 3 consensus framework H4

<400> 109
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1   5   10

<210> 113
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> CDP870 Light chain mature protein sequence

<400> 113
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
                20   25   30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
            35   40   45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
                100   105   110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
            115   120   125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130   135   140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145   150   155   160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165   170   175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180   185   190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
            195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 115
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> CDP870 Heavy chain mature protein sequence

<400> 115
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr

```
                 20                        25                        30
     Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met

                      35                        40                        45
     Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val
         50                        55                        60
     Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
     65                        70                        75                        80
     Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                      85                        90                        95
     Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
                     100                       105                       110
     Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
             115                       120                       125
     Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
         130                       135                       140
     Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
     145                       150                       155                       160
     Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                     165                       170                       175
     Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
                     180                       185                       190
     Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
             195                       200                       205
     Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
         210                       215                       220
     His Thr Cys Ala Ala
     225



     <210> 116
     <211> 1477
     <212> DNA
     <213> Artificial Sequence

     <220>
     <223> CDP870 nucleic acid sequence (sense strand)

     <400> 116
     atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac cgtagcgcaa   60
     gctgacattc aaatgaccca gagcccatcc agcctgagcg catctgtagg agaccgggtc  120
     accatcactt gtaaagccag tcagaacgta ggtactaacg tagcctggta tcagcaaaaa  180
     ccaggtaaag ccccaaaagc cctcatctac agtgcctctt cctctatag  tggtgtacca  240
     tacaggttca gcggatccgg tagtggtact gatttcaccc tcacgactag tagcctccag  300
     ccagaagatt tcgccactta ttactgtcaa cagtataaca tctacccact cacattcggt  360
     cagggtacta agtagaaat caaacgtacg gtagcggccc catctgtctt catcttcccg  420
     ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc  480
     tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc  540
     caggagagtg tcacagagca ggacagcaag acagcacct  acagcctcag cagcaccctg  600
     acgctgagga aagcagacta cgagaaacac aaagcttacg cctgcgaagt cacccatcag  660
     ggcctgagct caccagtaac aaaaagcttt aatagaggag agtgttgagg aggaaaaaaa  720
     aatgaagaaa actgctatag caattgcagt ggcgctagct ggtttcgcca ccgtggcgca  780
     agctgaggtt cagctggtcg agtcaggagg cggtctcgtg cagcctggcg atcactgag   840
     attgtcctgt gctgcatctg gttacgtctt cacagactat ggaatgaatt gggttagaca  900
     ggccccggga aagggcctcg aatggatggg ttggattaat acttacattg agagcctat   960
     ttatgctgac agcgtcaagg cgagattcac gttctctcta gacacatcca agtcaacagc 1020
     atacctccaa atgaatagcc tgagagcaga ggacaccgca gtgtactatt gtgctagagg 1080
```

atacagatct tatgccatgg actactgggg ccagggtacc ctagtcacag tctcctcagc 1140
ttccaccaag ggcccatcgg tcttcccct ggcaccctcc tccaagagca cctctggggg 1200
cacagcggcc ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg 1260
gaactcaggc gccctgacca gcggcgtgca caccttcccg ctgtcctac agtcctcagg 1320
actctactcc ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta 1380

catctgcaac gtgaatcaca gcccagcaa caccaaggtc cacaagaaag ttgagcccaa 1440
atcttgtgac aaaactcaca catgcgccgc gtgatga   1477

<210> 117
<211> 1477
<212> DNA
<213> Artificial Sequence

<220>
<223> CDP870 nucleic acid sequence (anti-sense strand)

<400> 117
tcatcacgcg gcgcatgtgt gagtttgtc acaagatttg ggctcaactt tcttgtggac 60
cttggtgttg ctgggcttgt gattcacgtt gcagatgtag gtctgggtgc ccaagctgct 120
ggagggcacg gtcaccacgc tgctgaggga gtagagtcct gaggactgta ggacagccgg 180
gaaggtgtgc acgccgctgg tcaggggcgcc tgagttccac gacaccgtca ccggttcggg 240
gaagtagtcc ttgaccaggc agcccagggc cgctgtgccc ccagaggtgc tcttggagga 300
gggtgccagg gggaagaccg atgggcctt ggtggaagct gaggagactg tgactaggggt 360
accctggccc cagtagtcca tggcataaga tctgtatcct ctagcacaat agtacactgc 420
ggtgtcctct gctctcaggc tattcatttg gaggtatgct gttgacttgg atgtgtctag 480
agagaacgtg aatctcgcct tgacgctgtc agcataaata ggctctccaa tgtaagtatt 540
aatccaaccc atccattcga ggccctttcc cggggcctgt ctaacccaat tcattccata 600
gtctgtgaag acgtaaccag atgcagcaca ggacaatctc agtgatccgc caggctgcac 660
gagaccgcct cctgactcga ccagctgaac ctcagcttgc gccacggtgg cgaaaccagc 720
tagcgccact gcaattgcta tagcagtttt cttcattttt ttttcctcct caacactctc 780
ctctattaaa gctttttgtt actggtgagc tcaggccctg atgggtgact tcgcaggcgt 840
aagctttgtg tttctcgtag tctgctttcc tcagcgtcag ggtgctgctg aggctgtagg 900
tgctgtcctt gctgtcctgc tctgtgacac tctcctggga gttacccgat tggagggcgt 960
tatccacctt ccactgtact ttggcctctc tgggatagaa gttattcagc aggcacacaa 1020
cagaggcagt tccagatttc aactgctcat cagatggcgg gaagatgaag acagatgggg 1080
ccgctaccgt acgtttgatt tctactttag taccctgacc gaatgtgagt gggtagatgt 1140
tatactgttg acagtaataa gtggcgaaat cttctggctg gaggctacta gtcgtgaggg 1200
tgaaatcagt accactaccg gatccgctga acctgtatgg tacaccacta tagaggaaag 1260
aggcactgta gatgagggct tttggggctt tacctggttt ttgctgatac caggctacgt 1320
tagtacctac gttctgactg gctttacaag tgatggtgac ccggtctcct acagatgcgc 1380
tcaggctgga tgggctctgg gtcatttgaa tgtcagcttg cgctacggta gcgaaaccag 1440
ccaaggccac tgcaattgcg atagctgtct ttttcat   1477